

#6

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/520,783  
Source: PG/10  
Date Processed by STIC: 1/19/05

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 01/19/2005

PATENT APPLICATION: US/10/520,783

TIME: 12:00:55

Input Set : A:\3083us0p.seq.txt

Output Set: N:\CRF4\01192005\J520783.raw

3 <110> APPLICANT: MATSUZAWA, Yuji  
 4 FUNAHASHI, Toru  
 5 SHIMOMURA, Ichirou  
 6 FURUYAMA, Naoki  
 8 <120> TITLE OF INVENTION: Novel Proteins and Use Thereof  
 10 <130> FILE REFERENCE: 3083USOP  
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/520,783  
 C--> 12 <141> CURRENT FILING DATE: 2005-01-10  
 12 <150> PRIOR APPLICATION NUMBER: PCT/JP03/08690  
 13 <151> PRIOR FILING DATE: 2003-07-09  
 15 <150> PRIOR APPLICATION NUMBER: JP 2002-201856  
 16 <151> PRIOR FILING DATE: 2002-07-10  
 18 <160> NUMBER OF SEQ ID NOS: 48  
 20 <170> SOFTWARE: PatentIn version 3.1  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 1836  
 24 <212> TYPE: DNA  
 25 <213> ORGANISM: Mus musculus  
 27 <220> FEATURE:  
 28 <221> NAME/KEY: CDS  
 29 <222> LOCATION: (1)..(1833)  
 30 <223> OTHER INFORMATION:  
 32 <220> FEATURE:  
 33 <221> NAME/KEY: sig\_peptide  
 34 <222> LOCATION: (1)..(69)  
 35 <223> OTHER INFORMATION:  
 W--> 37 <220>  
 38 <221> NAME/KEY: mat\_peptide  
 39 <222> LOCATION: (70)..()  
 40 <223> OTHER INFORMATION:  
 W--> 42 <220>  
 43 <221> NAME/KEY: misc\_feature  
 44 <222> LOCATION: (798)..(798)  
 45 <223> OTHER INFORMATION: 'n' stands for unidentified base.  
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 50 Met Ala Gly Ser Arg Gly Leu Pro Leu Leu Leu Val Leu Gln Leu  
 51 -20 -15 -10  
 53 ttc ctg ggc cct gtg ctg cct gtg agg gca cct gtg ttt ggc cga agt 96  
 54 Phe Leu Gly Pro Val Leu Pro Val Arg Ala Pro Val Phe Gly Arg Ser  
 55 -5 -1 1 5  
 57 gac acc ccc acc ctg agc ccc gag gag aat gaa ttt gtg gag gaa gag 144  
 58 Asp Thr Pro Thr Leu Ser Pro Glu Glu Asn Glu Phe Val Glu Glu Glu

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	59	10				15				20				25				
	61	aat	cag	cca	gtg	ctg	gtt	ctg	agc	tcc	gag	gag	cca	gag	cct	ggc	cca	192
	62	Asn	Gln	Pro	Val	Leu	Val	Leu	Ser	Ser	Glu	Glu	Pro	Glu	Pro	Gly	Pro	
	63					30					35				40			
	65	gcc	act	gtc	gac	tgt	ccc	cga	gat	tgt	gcc	tgt	tcc	cag	gaa	ggg	gta	240
	66	Ala	Thr	Val	Asp	Cys	Pro	Arg	Asp	Cys	Ala	Cys	Ser	Gln	Glu	Gly	Val	
	67				45					50				55				
	69	gtg	gac	tgt	ggg	ggc	att	gac	ctg	cgt	gag	ttt	cca	ggc	gac	ctg	ccc	288
	70	Val	Asp	Cys	Gly	Gly	Ile	Asp	Leu	Arg	Glu	Phe	Pro	Gly	Asp	Leu	Pro	
	71			60					65				70					
	73	gag	cac	acc	aac	cat	ctc	tcc	ttg	cag	aac	aac	cag	ctg	gag	aag	atc	336
	74	Glu	His	Thr	Asn	His	Leu	Ser	Leu	Gln	Asn	Asn	Gln	Leu	Glu	Lys	Ile	
	75		75					80					85					
	77	tac	ccc	gag	gag	ctg	tcc	cgg	ctg	cag	cgg	ctg	gag	acg	ctg	aac	ctg	384
	78	Tyr	Pro	Glu	Glu	Leu	Ser	Arg	Leu	Gln	Arg	Leu	Glu	Thr	Leu	Asn	Leu	
	79	90					95					100					105	
	81	cag	aac	aac	cgc	ctg	aca	tcc	cga	ggg	ctc	cca	gag	gag	gca	ttt	gag	432
	82	Gln	Asn	Asn	Arg	Leu	Thr	Ser	Arg	Gly	Leu	Pro	Glu	Glu	Ala	Phe	Glu	
	83					110					115				120			
	85	cat	ctt	act	agc	ctc	aat	tac	ctg	tac	ctg	gcc	aac	aac	aag	ctg	aca	480
	86	His	Leu	Thr	Ser	Leu	Asn	Tyr	Leu	Tyr	Leu	Ala	Asn	Asn	Lys	Leu	Thr	
	87				125					130					135			
	89	ctg	gca	ccc	cga	ttc	ctg	cca	aac	gcc	ctg	atc	agt	gtg	gac	ttt	gct	528
	90	Leu	Ala	Pro	Arg	Phe	Leu	Pro	Asn	Ala	Leu	Ile	Ser	Val	Asp	Phe	Ala	
	91			140					145				150					
	93	gcc	aat	tat	ctc	act	aag	atc	tat	gga	ctc	acc	ttt	ggc	caa	aag	cca	576
	94	Ala	Asn	Tyr	Leu	Thr	Lys	Ile	Tyr	Gly	Leu	Thr	Phe	Gly	Gln	Lys	Pro	
	95		155					160				165						
	97	aat	ctg	agg	tct	gtg	tac	ctg	cat	aac	aac	aag	cta	gca	gat	gcc	ggg	624
	98	Asn	Leu	Arg	Ser	Val	Tyr	Leu	His	Asn	Asn	Lys	Leu	Ala	Asp	Ala	Gly	
	99	170					175					180					185	
	101	ctg	ccg	gac	cac	atg	ttc	aat	ggc	tcc	agc	aac	gtc	gag	atc	cta	atc	672
	102	Leu	Pro	Asp	His	Met	Phe	Asn	Gly	Ser	Ser	Asn	Val	Glu	Ile	Leu	Ile	
	103					190						195				200		
	105	ctg	tcc	agc	aac	ttc	ctg	cgc	cat	gtg	ccc	aag	cac	ctg	cca	ccc	gct	720
	106	Leu	Ser	Ser	Asn	Phe	Leu	Arg	His									

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125	cca	gcg	ggt	ctt	ccc	cgc	agc	ctg	gtc	ctg	ctg	cac	ctg	gag	aaa	aat	960
126	Pro	Ala	Gly	Leu	Pro	Arg	Ser	Leu	Val	Leu	Leu	His	Leu	Glu	Lys	Asn	
127				285					290					295			
129	gcc	atc	cag	agc	gta	gaa	gct	gat	gtg	ctg	aca	ccc	atc	cgc	aac	ctg	1008
130	Ala	Ile	Gln	Ser	Val	Glu	Ala	Asp	Val	Leu	Thr	Pro	Ile	Arg	Asn	Leu	
131			300					305					310				
133	gag	tac	ctg	ctg	cta	cat	agc	aac	cag	ctg	cag	gcc	aag	ggt	atc	cac	1056
134	Glu	Tyr	Leu	Leu	Leu	His	Ser	Asn	Gln	Leu	Gln	Ala	Lys	Gly	Ile	His	
135		315					320					325					
137	cca	ctg	gcc	ttc	cag	ggc	ctc	aag	aag	ctc	cac	aca	gtg	cat	cta	tac	1104
138	Pro	Leu	Ala	Phe	Gln	Gly	Leu	Lys	Lys	Leu	His	Thr	Val	His	Leu	Tyr	
139	330					335						340				345	
141	aac	aac	gcg	ctg	gaa	cgt	gtg	ccc	agc	ggc	ctg	ccc	cgc	cga	gtg	cgc	1152
142	Asn	Asn	Ala	Leu	Glu	Arg	Val	Pro	Ser	Gly	Leu	Pro	Arg	Arg	Val	Arg	
143				350						355					360		
145	acc	ctc	atg	atc	ctg	cac	aac	cag	att	aca	ggc	ata	ggc	cgt	gag	gac	1200
146	Thr	Leu	Met	Ile	Leu	His	Asn	Gln	Ile	Thr	Gly	Ile	Gly	Arg	Glu	Asp	
147			365						370				375				
149	ttc	gct	acc	acc	tac	ttc	ctg	gaa	gag	ctc	aac	ctc	agc	tac	aac	cgc	1248
150	Phe	Ala	Thr	Thr	Tyr	Phe	Leu	Glu	Glu	Leu	Asn	Leu	Ser	Tyr	Asn	Arg	
151			380					385					390				
153	atc	acc	agc	cca	cag	atg	cac	cga	gat	gcc	ttc	cgc	aag	cta	cgc	ctg	1296
154	Ile	Thr	Ser	Pro	Gln	Met	His	Arg	Asp	Ala	Phe	Arg	Lys	Leu	Arg	Leu	
155		395					400					405					
157	ctg	cgt	tca	ctt	gac	ttg	tct	ggc	aac	cgt	ctg	caa	aca	ctg	cct	cca	1344
158	Leu	Arg	Ser	Leu	Asp	Leu	Ser	Gly	Asn	Arg	Leu	Gln	Thr	Leu	Pro	Pro	
159	410				415						420				425		
161	ggc	ctg	ccg	aaa	aac	gta	cac	gtg	ctc	aag	gtc	aag	cgg	aat	gag	ctg	1392
162	Gly	Leu	Pro	Lys	Asn	Val	His	Val	Leu	Lys	Val	Lys	Arg	Asn	Glu	Leu	
163				430						435					440		
165	gct	gcc	ctg	gca	cgt	ggg	gca	cta	gct	ggc	atg	gcc	cag	ctt	cgg	gaa	1440
166	Ala	Ala	Leu	Ala	Arg	Gly	Ala	Leu	Ala	Gly	Met	Ala	Gln	Leu	Arg	Glu	
167			445					450					455				
169	ctc	tac	ctc	aca	ggc	aac	cga	ctg	cga	agc	cgg	gcc	ctg	gga	ccc	cgt	1488
170	Leu	Tyr	Leu	Thr	Gly	Asn	Arg	Leu	Arg	Ser	Arg	Ala	Leu	Gly	Pro	Arg	
171			460					465					470				
173	gcc	tgg	gtg	gac	ctt	gct	ggt	ctg	cag	ctg	ctg	gac	atc	gct	ggg	aat	1536
174	Ala	Trp	Val	Asp	Leu	Ala	Gly	Leu	Gln	Leu	Leu	Asp	Ile	Ala	Gly	Asn	
175		475					480					485					
177	cag	ctc	aca	gag	gtc	cct	gag	ggg	ctc	ccc	cca	tct	ctg	gag	tat	ctg	1584
178	Gln	Leu	Thr	Glu	Val	Pro	Glu	Gly	Leu	Pro	Pro	Ser	Leu	Glu	Tyr	Leu	
179	490					495					500				505		
181	tac	ctg	cag	aat	aac	aag	att	agt	gcc	gtt	cct	gcc	aac	gcc	ttt	gac	1632
182	Tyr	Leu	Gln	Asn	Asn	Lys	Ile	Ser	Ala	Val	Pro	Ala	Asn	Ala	Phe	Asp	
183				510						515					520		
185	tcc	act	ccc	aac	ctt	aag	ggg	atc	ttt	ctc	agg	ttc	aac	aag	ctg	gct	1680
186	Ser	Thr	Pro	Asn	Leu	Lys	Gly	Ile	Phe	Leu	Arg	Phe	Asn	Lys	Leu	Ala	
187				525						530				535			
189	gtg	ggc	tcc	gtg	gtg	gaa	agc	gcc	ttc	cgg	agg	ctg	aaa	cac	ctg	cag	1728

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190 Val Gly Ser Val Val Glu Ser Ala Phe Arg Arg Leu Lys His Leu Gln
191          540          545          550
193 gtc ttg gac att gaa ggc aac ttt gag ttt ggt aat ggt tcc aag gac      1776
194 Val Leu Asp Ile Glu Gly Asn Phe Glu Phe Gly Asn Gly Ser Lys Asp
195          555          560          565
197 aaa gat gag gaa gag gaa gaa gag gag gaa gag gaa gat gag gaa gag      1824
198 Lys Asp Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu Glu Glu
199 570          575          580          585
201 gaa act aga tag      1836
202 Glu Thr Arg
206 <210> SEQ ID NO: 2
207 <211> LENGTH: 611
208 <212> TYPE: PRT
209 <213> ORGANISM: Mus musculus
211 <400> SEQUENCE: 2
213 Met Ala Gly Ser Arg Gly Leu Pro Leu Leu Leu Leu Val Leu Gln Leu
214          -20          -15          -10
217 Phe Leu Gly Pro Val Leu Pro Val Arg Ala Pro Val Phe Gly Arg Ser
218          -5          -1 1          5
221 Asp Thr Pro Thr Leu Ser Pro Glu Glu Asn Glu Phe Val Glu Glu Glu
222 10          15          20          25
225 Asn Gln Pro Val Leu Val Leu Ser Ser Glu Glu Pro Glu Pro Gly Pro
226          30          35          40
229 Ala Thr Val Asp Cys Pro Arg Asp Cys Ala Cys Ser Gln Glu Gly Val
230          45          50          55
233 Val Asp Cys Gly Gly Ile Asp Leu Arg Glu Phe Pro Gly Asp Leu Pro
234          60          65          70
237 Glu His Thr Asn His Leu Ser Leu Gln Asn Asn Gln Leu Glu Lys Ile
238          75          80          85
241 Tyr Pro Glu Glu Leu Ser Arg Leu Gln Arg Leu Glu Thr Leu Asn Leu
242 90          95          100          105
245 Gln Asn Asn Arg Leu Thr Ser Arg Gly Leu Pro Glu Glu Ala Phe Glu
246          110          115          120
249 His Leu Thr Ser Leu Asn Tyr Leu Tyr Leu Ala Asn Asn Lys Leu Thr
250          125          130          135
253 Leu Ala Pro Arg Phe Leu Pro Asn Ala Leu Ile Ser Val Asp Phe Ala
254          140          145          150
257 Ala Asn Tyr Leu Thr Lys Ile Tyr Gly Leu Thr Phe Gly Gln Lys Pro
258          155          160          165
261 Asn Leu Arg Ser Val Tyr Leu His Asn Asn Lys Leu Ala Asp Ala Gly
262 170          175          180          185
265 Leu Pro Asp His Met Phe Asn Gly Ser Ser Asn Val Glu Ile Leu Ile
266          190          195          200
269 Leu Ser Ser Asn Phe Leu Arg His Val Pro Lys His Leu Pro Pro Ala
270          205          210          215
273 Leu Tyr Lys Leu His Leu Lys Asn Asn Lys Leu Glu Lys Ile Pro Pro
274          220          225          230
277 Gly Ala Phe Ser Glu Leu Ser Asn Leu Arg Glu Leu Tyr Leu Gln Asn
278          235          240          245

```

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Input Set : A:\3083us0p.seq.txt

Output Set: N:\CRF4\01192005\J520783.raw

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281 Asn Tyr Leu Thr Asp Glu Gly Leu Asp Asn Glu Thr Phe Trp Lys Leu
282 250                255                260                265
285 Ser Ser Leu Glu Tyr Leu Asp Leu Ser Ser Thr Asn Leu Ser Arg Val
286                270                275                280
289 Pro Ala Gly Leu Pro Arg Ser Leu Val Leu Leu His Leu Glu Lys Asn
290                285                290                295
293 Ala Ile Gln Ser Val Glu Ala Asp Val Leu Thr Pro Ile Arg Asn Leu
294                300                305                310
297 Glu Tyr Leu Leu Leu His Ser Asn Gln Leu Gln Ala Lys Gly Ile His
298                315                320                325
301 Pro Leu Ala Phe Gln Gly Leu Lys Lys Leu His Thr Val His Leu Tyr
302 330                335                340                345
305 Asn Asn Ala Leu Glu Arg Val Pro Ser Gly Leu Pro Arg Arg Val Arg
306                350                355                360
309 Thr Leu Met Ile Leu His Asn Gln Ile Thr Gly Ile Gly Arg Glu Asp
310                365                370                375
313 Phe Ala Thr Thr Tyr Phe Leu Glu Glu Leu Asn Leu Ser Tyr Asn Arg
314                380                385                390
317 Ile Thr Ser Pro Gln Met His Arg Asp Ala Phe Arg Lys Leu Arg Leu
318                395                400                405
321 Leu Arg Ser Leu Asp Leu Ser Gly Asn Arg Leu Gln Thr Leu Pro Pro
322 410                415                420                425
325 Gly Leu Pro Lys Asn Val His Val Leu Lys Val Lys Arg Asn Glu Leu
326                430                435                440
329 Ala Ala Leu Ala Arg Gly Ala Leu Ala Gly Met Ala Gln Leu Arg Glu
330                445                450                455
333 Leu Tyr Leu Thr Gly Asn Arg Leu Arg Ser Arg Ala Leu Gly Pro Arg
334                460                465                470
337 Ala Trp Val Asp Leu Ala Gly Leu Gln Leu Leu Asp Ile Ala Gly Asn
338                475                480                485
341 Gln Leu Thr Glu Val Pro Glu Gly Leu Pro Pro Ser Leu Glu Tyr Leu
342 490                495                500                505
345 Tyr Leu Gln Asn Asn Lys Ile Ser Ala Val Pro Ala Asn Ala Phe Asp
346                510                515                520
349 Ser Thr Pro Asn Leu Lys Gly Ile Phe Leu Arg Phe Asn Lys Leu Ala
350                525                530                535
353 Val Gly Ser Val Val Glu Ser Ala Phe Arg Arg Leu Lys His Leu Gln
354                540                545                550
357 Val Leu Asp Ile Glu Gly Asn Phe Glu Phe Gly Asn Gly Ser Lys Asp
358                555                560                565
361 Lys Asp Glu Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu Glu Glu
362 570                575                580                585
365 Glu Thr Arg
369 <210> SEQ ID NO: 3
370 <211> LENGTH: 480
371 <212> TYPE: DNA
372 <213> ORGANISM: Mus musculus
374 <220> FEATURE:
375 <221> NAME/KEY: CDS

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**RAW SEQUENCE LISTING ERROR SUMMARY**

DATE: 01/19/2005

PATENT APPLICATION: US/10/520,783

TIME: 12:00:56

Input Set : A:\3083us0p.seq.txt

Output Set: N:\CRF4\01192005\J520783.raw

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 798

Seq#:23; N Pos. 633,680,682

Seq#:25; N Pos. 662

Seq#:27; N Pos. 325,329

Seq#:29; N Pos. 605

Seq#:30; N Pos. 589

## VERIFICATION SUMMARY

DATE: 01/19/2005

PATENT APPLICATION: US/10/520,783

TIME: 12:00:56

Input Set : A:\3083us0p.seq.txt

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:37 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:30  
L:42 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:35  
L:48 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:40  
L:113 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:768  
L:384 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:377  
L:389 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:382  
L:389 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:387  
L:493 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:486  
L:498 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:491  
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L:706 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:699  
L:711 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:704  
L:711 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:709  
L:903 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:896  
L:908 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:901  
L:908 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:906  
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L:2028 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:21,Line#:2021  
L:2028 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:21,Line#:2026  
L:2609 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:600  
M:341 Repeated in SeqNo=23  
L:2675 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:660  
L:2751 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:300  
L:2827 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:600  
L:2870 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:540  
L:3094 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:47